ECEC21
Session 2B: Detection, Fate, and Transport of PFAS 2
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Microbiological Signature of PFAS-laden Surface Water Foams

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EGLE
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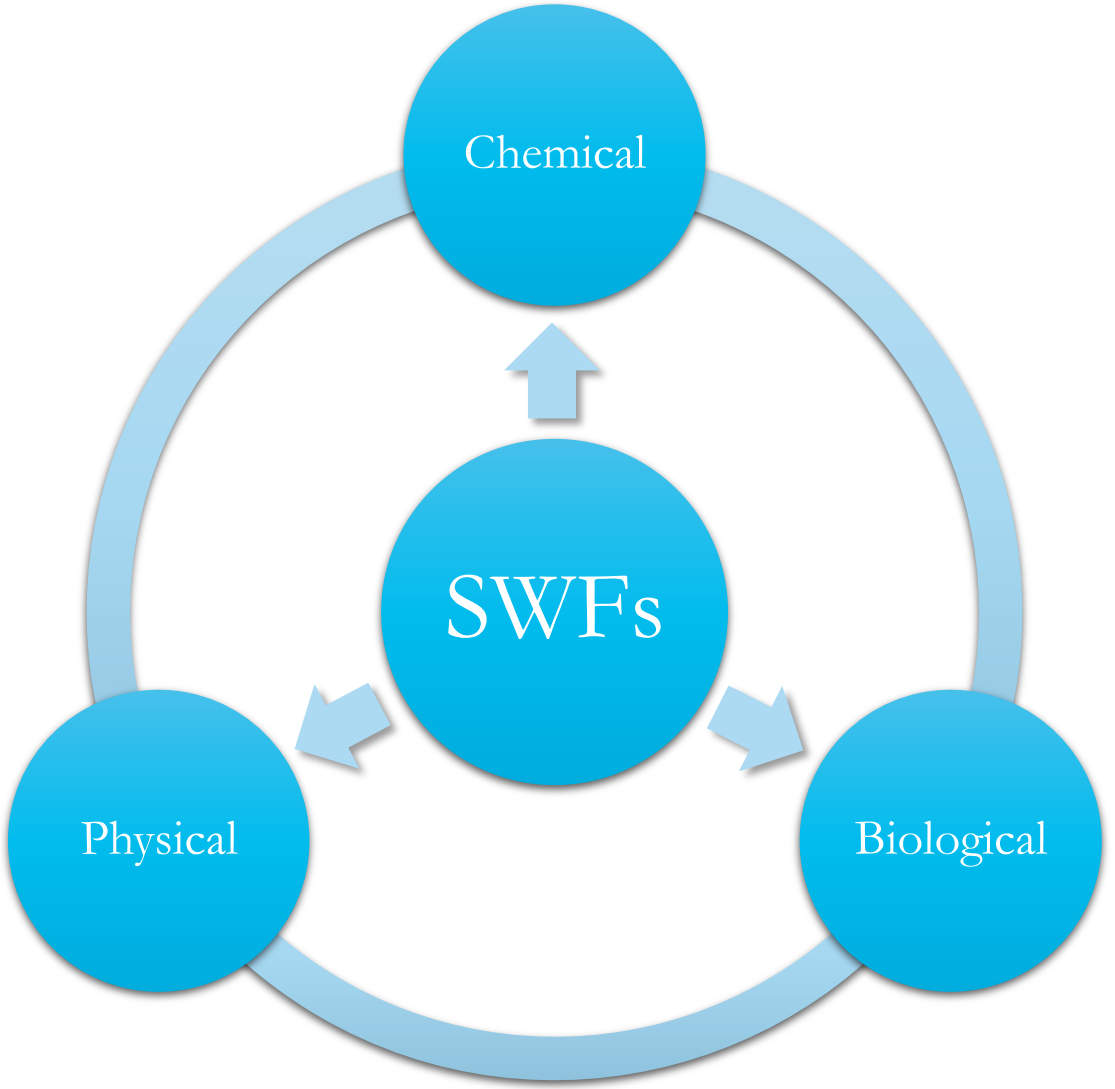
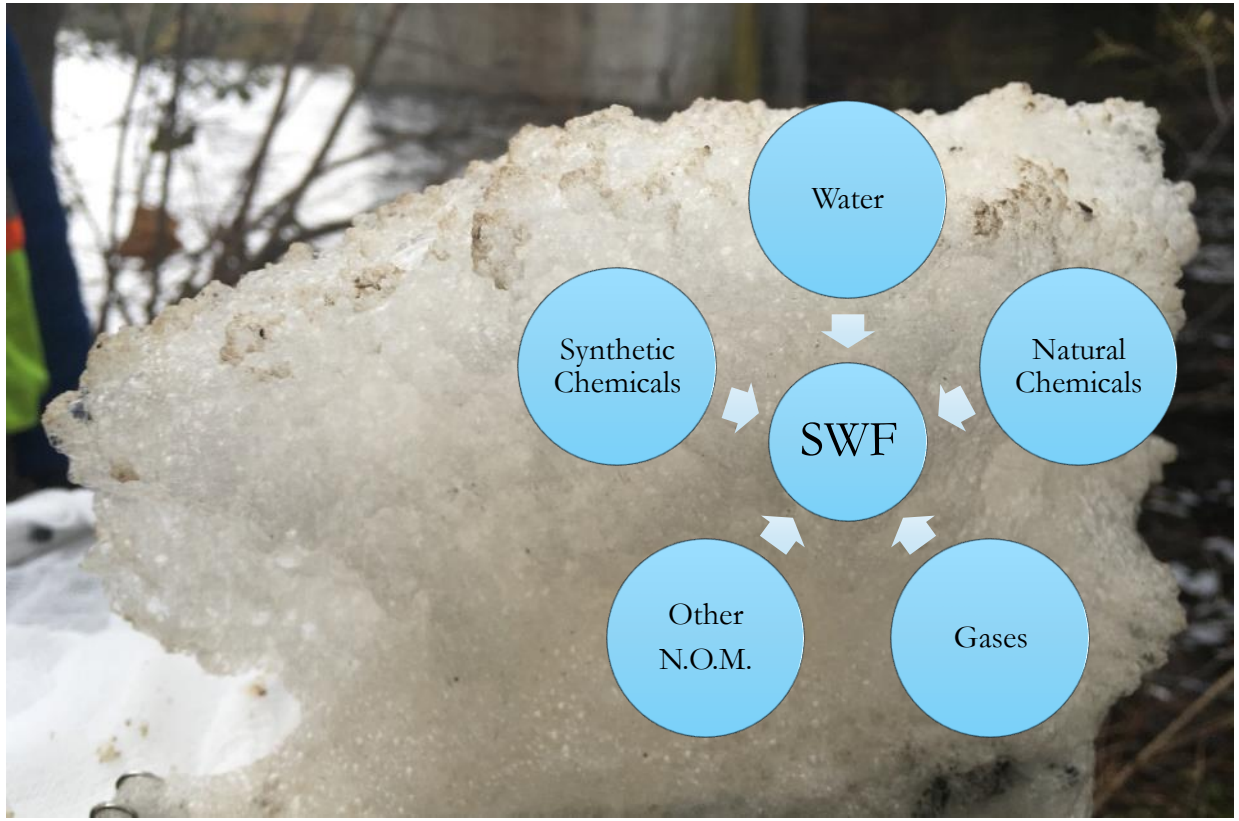
Context

- Michigan Department of Environment, Great Lakes, and Energy (EGLE) & Michigan PFAS Action Response Team (MPART).
- Field Work 2019-2021: Four rivers & three inland lakes.
- First study using extended 41-list of PFAS and Metagenomic Sequencing of SWF.
- AECOM *Surface Water Foam Study Report*, Michigan EGLE, January 7, 2021.



Surface Water Foams (SWFs)

- Can be natural or of human origin or both,
- Globally widespread and form in marine, brackish and freshwater habitats,
- Compositionally are made of water, gases, and mineral fractions, with traces of natural and synthetic chemicals and biological components,
- Genesis, occurrence, fate and transport are on-going study topics by many researchers.



Stable SWF collected from the Rogue River, Michigan [11/04/19].

Precedence: Biodegradation of PFAS

Organism	Compounds	Process	Reference
Pseudomonas parafulva	PFOS, PFOA	Degradation	Yi, et al., 2018
Pseudomonas aeruginosa	PFOS	Degradation	Kwon, et al., 2019
Pseudomonas plecoglossicida	PFOS	Degradation	Chetverikov, et al., 2017
Acidimicrobium sp. strain A6	PFOS, PFOA	Degradation/Defluorination	Huang & Jaffé, 2019
Pseudomonas [striata] strain PS27 *[Burkholderia cenocepacia* strain PS27]	PFHxS	Bioaccumulation	Presentato, et al., 2020
Pseudomonas sp. strain PDMF10	PFHxS	Bioaccumulation	Presentato, et al., 2020
Gordonia sp. strain NB4-1Y	6:2 FTSA	Degradation	Shaw, et al., 2019
Desulfococcus	Total PFAS	Positive Correlation	O'Carroll, et al., 2020
Oxalobacteraceae	Total PFAS	Negative Correlation	O'Carroll, et al., 2020
Syntrophaceae	Total PFAS	Positive Correlation	O'Carroll, et al., 2020
Gordonia sp., Nitrosomas, Rhodococcus	4:2, 6:2, 8:2 FTSA	Transformation	Harding-Marjanovic, et al., 2015
Various Fungi [Laccase]	PFOA	Laccase Catalysis Degradation	Luo, et al., 2015

SWF Sampling Approach

- Entire column of SWF collected with pool skimmer net.
- SWF transferred into 2-gal Ziploc® bags.

- SWF refrigerated and allowed to condense for 24hrs.
- Slowly poured through cheese cloth into sample bottles to strain out large debris.

- 20mL condensed SWF preserved for Shotgun Metagenomic Sequencing.
- ≥20mL condensed foam prepared for 41 PFAS analysis.

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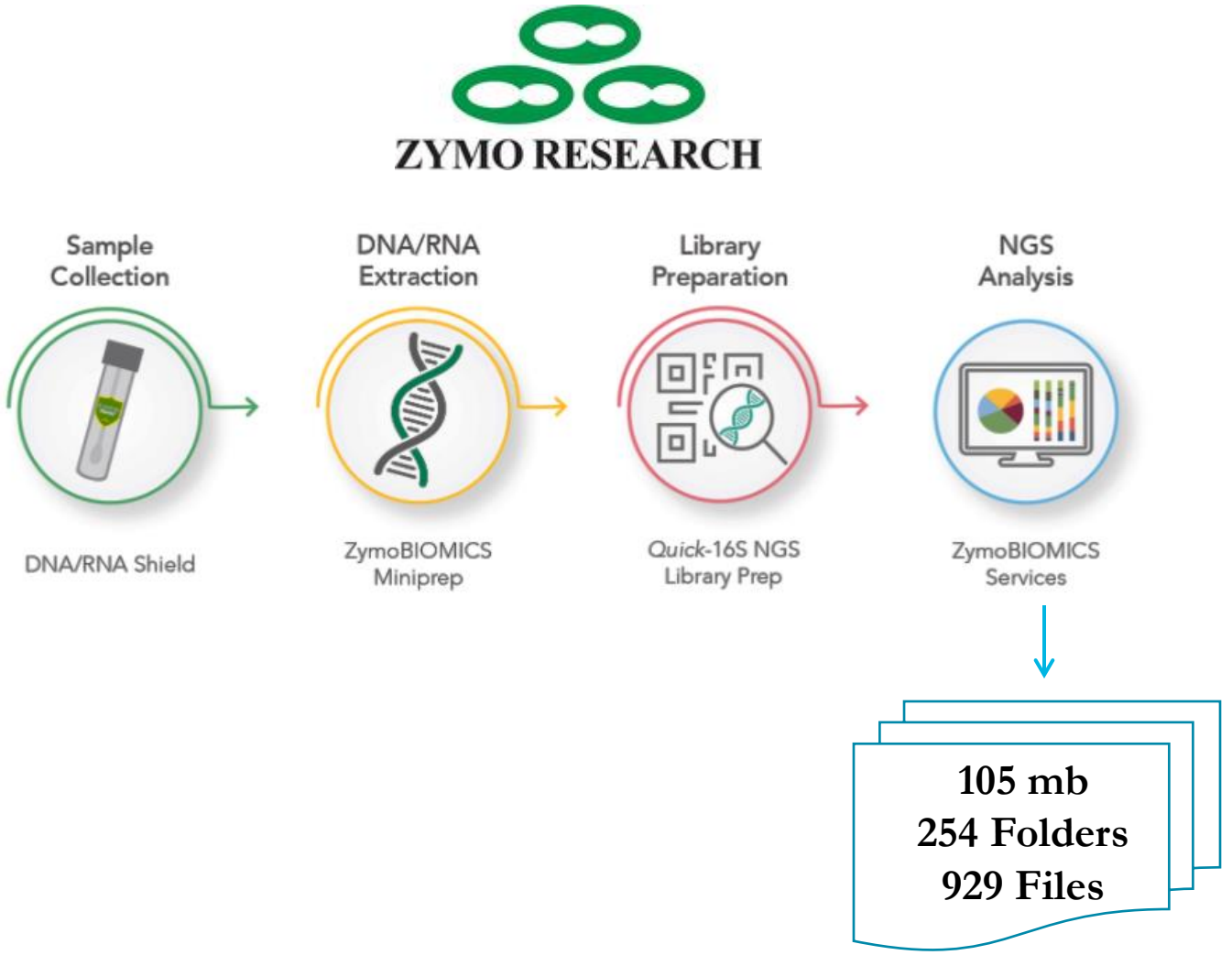
Shotgun Metagenomic Sequencing

- 15 SWF samples + 1 Duplicate
- ZymoBIOMICS®
  Zymo Research, Irvine, CA
- Prokaryotes, fungi, limited virus
- Nextera® DNA Flex Kit
- Illumina NovaSeq®
- Trimmomatic Software Tool
  DIAMOND Sequencer
  QIIME Pipeline
  DADA2



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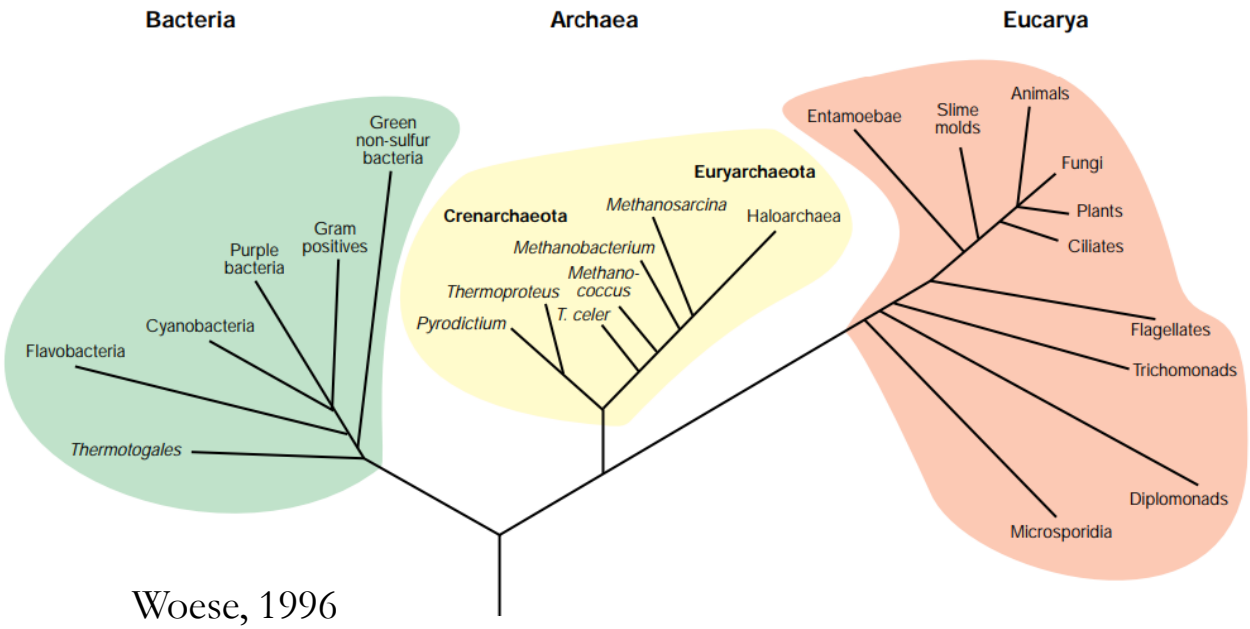
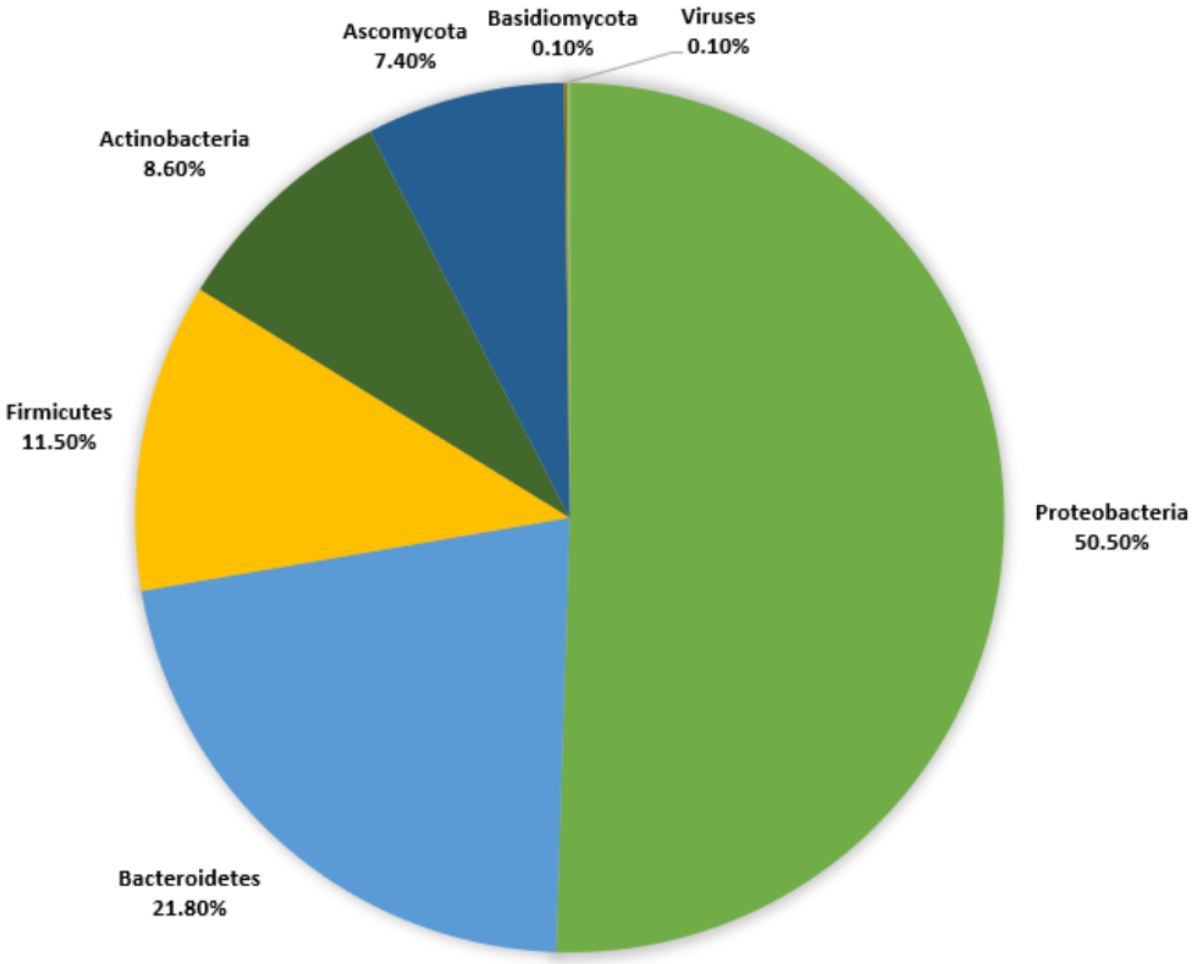
Predominant Phyla Identified in SWF

- Proteobacteria (50.5%)
- Bacteroidetes (21.8%); Firmicutes (11.5%)
- Actinobacteria (8.6%)
- Ascomycota – Fungi, including some yeasts



Woese, 1996



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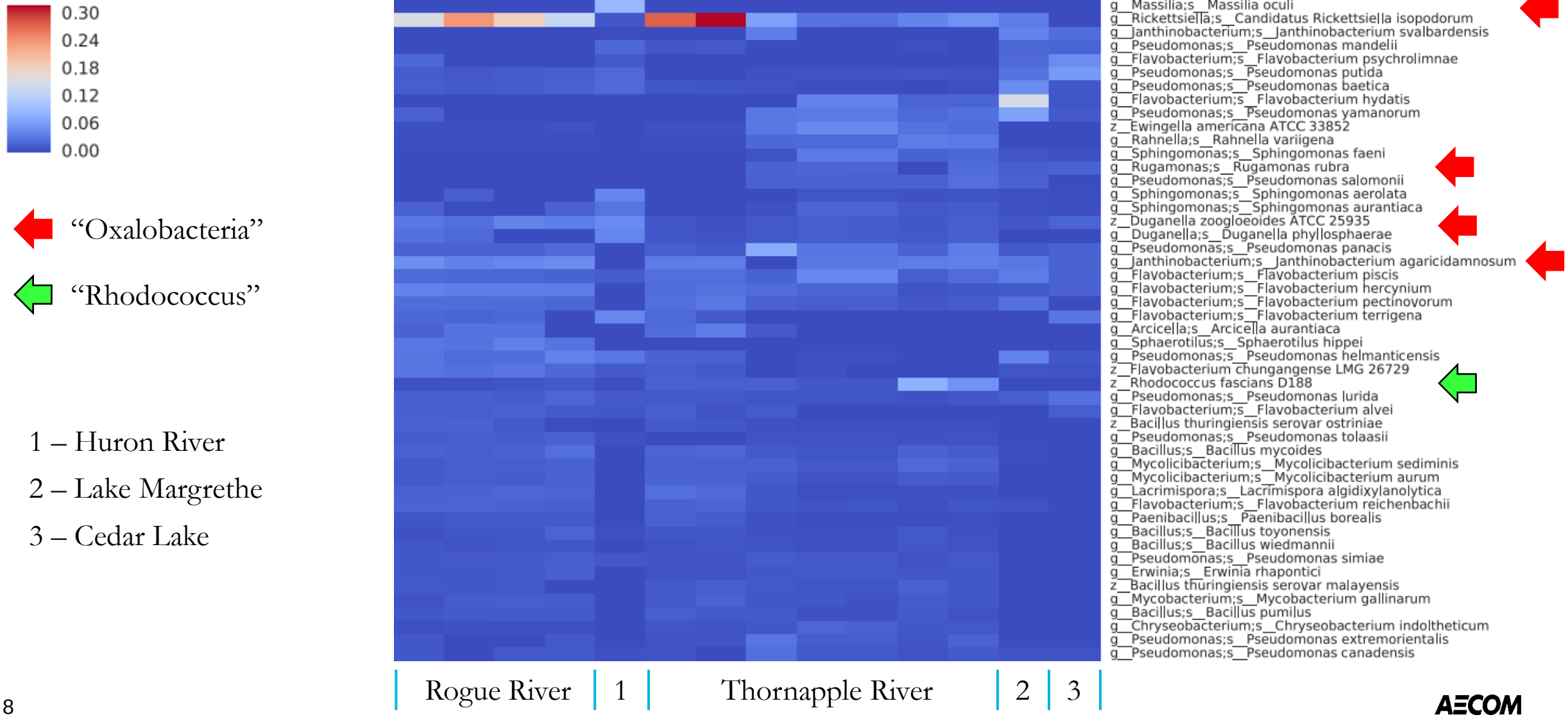
Phylogenetic Heat Map (Bacteria Strain Level)



"Oxalobacteria"

"Rhodococcus"

1 – Huron River

2 – Lake Margrethe

3 – Cedar Lake

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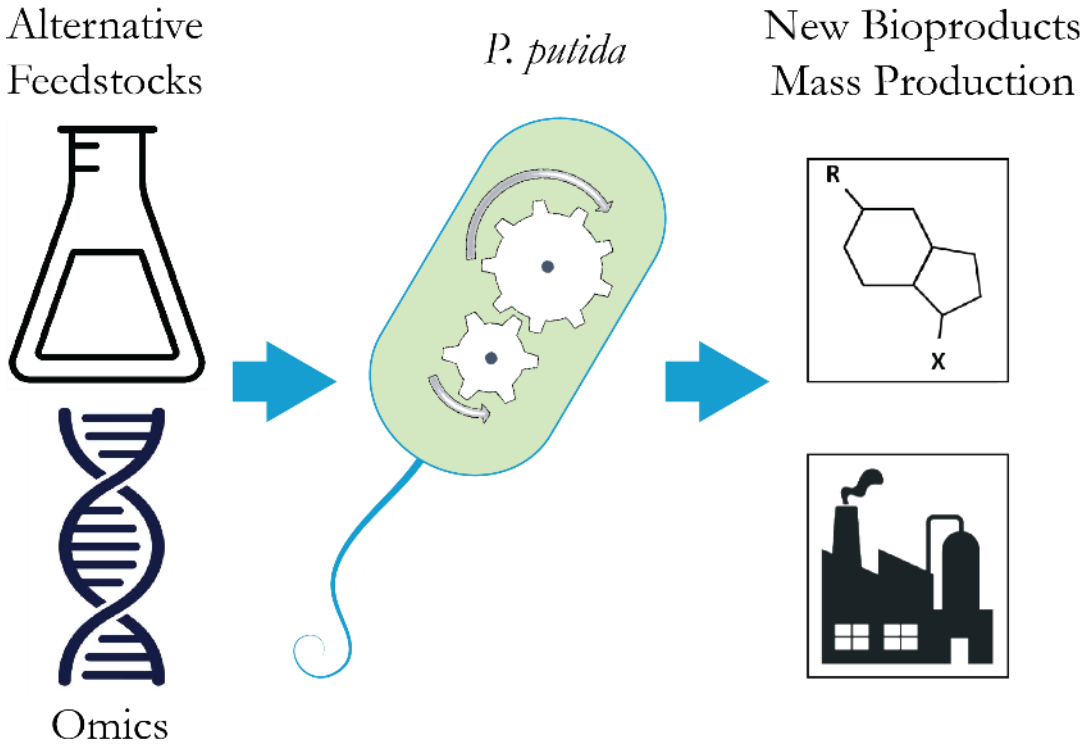
Pseudomonas sp.

- Common wide-spread genus of gram-negative gammaproteobacterial.
- Many documented as contaminant-dwellers and in bioremediation, including PFAS. Some produce biosurfactants.
- Have been identified in Feammox process (Sawayama, 2006).
- 191 validated species, some are now being lumped under *Burkholderia*.
- 63 species identified in SWF.
- *Pseudomonas lurida* found in all samples; *P. baetica, P. panicus, P. putida* and *P. helmanticensis* found in most of the samples.



Bacteria *P. Putida* as a functional chassis for creation of new biochemistries and products. Adapted from Nike & de Lorenzo, 2018.

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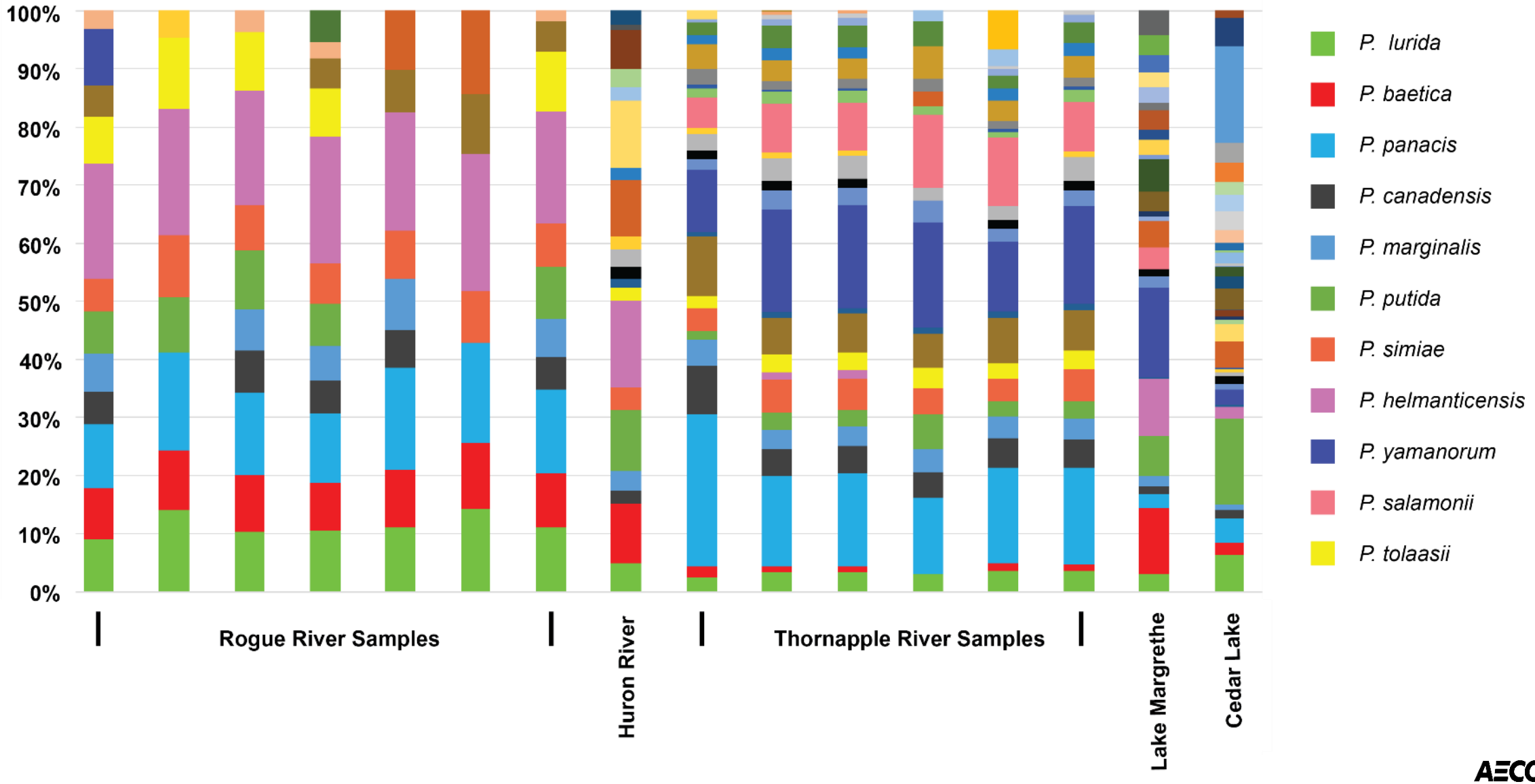
Predominant *Pseudomonas* in SWF



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Functional Genes

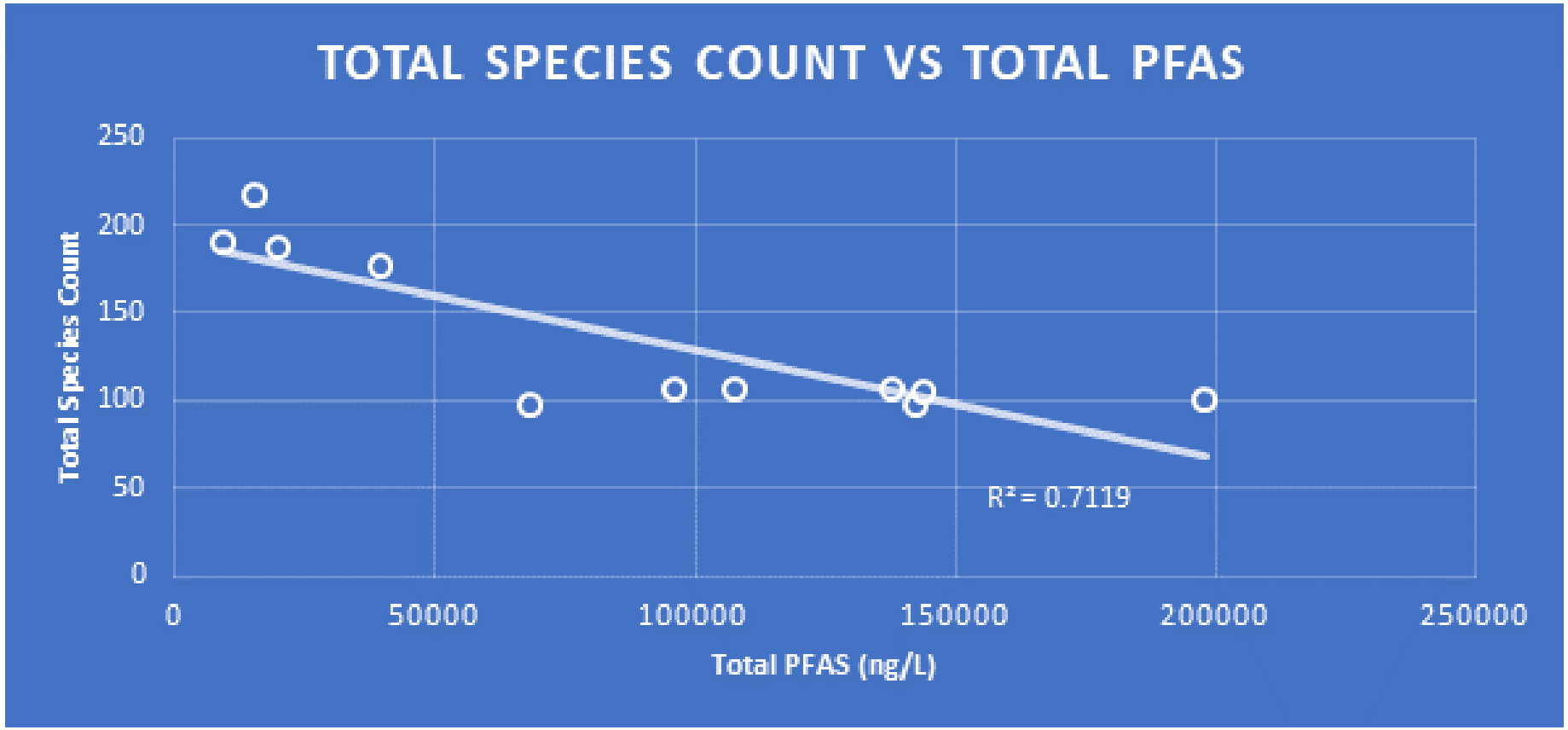
- Over 750 functional genes identified in SWF, the most common genes summarized below.
- Dehalogenation genes not identified.
- Heme-b biosynthesis, involves use of **Uroporphyrinogen Decarboxylase (UroD).**
  - Elimination of carboxyl groups; UroD performs decarboxylations without the intervention of any cofactors.
  - Considered the benchmark for catalytic efficiency in enzymes (Lewis & Wolfenden, 2008).

15 Samples

Functional Gene / Species	Occurrence
HISDEG-PWY: L-histidine degradation I	11.0
PWY-6151: S-adenosyl-L-methionine cycle I	11.0
PWY-7111: pyruvate fermentation to isobutanol (engineered)	11.0
VALSYN-PWY: L-valine biosynthesis	11.0
HEMESYN2-PWY: heme biosynthesis II (anaerobic)	10.0
HOMOSER-METSYN-PWY: L-methionine biosynthesis I	10.0
PEPTIDOGLYCANSYN-PWY: peptidoglycan biosynthesis I (meso-diaminopimelate containing)|g__Bacillus.s__Bacillus_cereus_thuringiensis	10.0
PWY0-1296: purine ribonucleosides degradation	10.0
PWY-6387: UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing)	10.0
HEME-BIOSYNTHESIS-II: heme biosynthesis I (aerobic)	9.0

Food for Fodder

Total Number of Bacteria Species in River SWF Plotted vs. Total PFAS Concentration (ng/L)



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Q & A

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THANK YOU

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